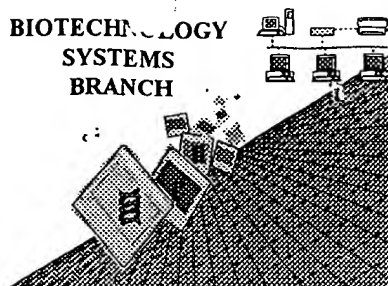


*Hayes*

**BEST AVAILABLE COPY**  
**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



*f#8*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/474,980A

Source: 1647

Date Processed by STIC: 3/22/2001

**RECEIVED**

APR 02 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/474,980A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                                 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
                                 This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

RAW SEQUENCE LISTING                      DATE: 03/22/2001  
 PATENT APPLICATION: US/09/474,980A                      TIME: 16:17:41

Input Set : A:\60292668.txt  
 Output Set: N:\CRF3\03222001\I474980A.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: JOHNSON Jr., Eugene M.  
 4        MILBRANDT, Jeffrey D.  
 5        KOTZBAUER, Paul T.  
 6        LAMPE, Patricia A.  
 7        KLEIN, Robert  
 8        DESAUVAGE, Fred  
 10 <120> TITLE OF INVENTION: Persephin and Related Growth Factors  
 12 <130> FILE REFERENCE: 6029-2668  
 14 <140> CURRENT APPLICATION NUMBER: 09/474,980A  
 15 <141> CURRENT FILING DATE: 1999-12-29  
 17 <150> PRIOR APPLICATION NUMBER: 08/519,777  
 18 <151> PRIOR FILING DATE: 1995-08-28  
 20 <160> NUMBER OF SEQ ID NOS: 242  
 22 <170> SOFTWARE: Microsoft Word 97

# ERRORED SEQUENCES

276 <210> SEQ ID NO: 11  
 277 <211> LENGTH: (591) 594 shown  
 278 <212> TYPE: DNA  
 279 <213> ORGANISM: Homo sapiens  
 281 <400> SEQUENCE: 11  
 282 atgcagcgct ggaaggcggc ggccttgcc tcagtgcctc gcagctccgt gctgtccatc 60  
 284 tggatgtgtc gagaggcct gcttctcagc caccgcctcg gacctgcgct ggtccccctg 120  
 286 caccgcctgc ctggaacctt gacgcccgg attgcccgc tggcccagta ccgtgcactc 180  
 288 ctgcaggggg ccccgatgc gatggagctg cgcgagctga cgcctggggc tggggggccc 240  
 290 ccagggtccg gccgtcggg ggggcccgg cggcgccgc cgcgtgcgcg gttggggggc 300  
 292 cggccttgcg ggtgcgcga gctggaggtg cgcgtgagcg agctgggctt gggctacgcg 360  
 294 tccgacgaga cgggtctgtt ccgctactgc gcaggcgcct gcgaggctgc cgcgcgcgtc 420  
 296 tacgacctcg ggtgcgcag actgcgccag cggcgccgc tgcggcggga gcgggtgcgc 480  
 298 gcgcagccct gctgccgcc gacggcctac gaggacgagg tgctcttctt ggacgcgcac 540  
 E--> 300 agccgctacc acacgggtga cgagctgtcg gcgcgcgagt gcgcctgcgt gtga 594  
 303 <210> SEQ ID NO: 12  
 304 <211> LENGTH: (585) 588 (next page)  
 305 <212> TYPE: DNA  
 306 <213> ORGANISM: Mus musculus  
 308 <400> SEQUENCE: 12  
 309 atgaggcgct ggaaggcagc ggccttggtg tcgctcatct gcagctccct gctatctgtc 60  
 311 tggatgtgtc aggagggtct gctcttgggc caccgcctgg gaccgcgcct tgcgccgcta 120  
 313 cgacgccttc cagcacctt ggaagccgc atcgcccgc tggcccagta tcgcgctctg 180  
 315 ctccaggggc ccccgacgc ggtggagctt cgagaacttt ctccctgggc tgcgcgcac 240  
 317 ccgggaccgc gccgtcgagc ggttccccgg cgtcggcggg cgcggccggg ggtcggcct 300  
 319 tgtgggctgc gcgagctcga ggtgcgcgtg agcgagctgg gcctgggcta cagtcggat 360  
 321 gagaccgtgc tgttccgcta ctgcgcaggc gcgtgcgagg cggccatccg catctacgac 420  
 323 ctgggcttct ggcgcctcgc ccagcggagg cgcgtgcgca gagagcgggc gcgggcgcac 480  
 325 ccgtgttgtc gcccgacggc ctatgaggac gaggtgtcct tcctggacgt gcacagccgc 540

## RAW SEQUENCE LISTING

DATE: 03/22/2001

PATENT APPLICATION: US/09/474,980A

TIME: 16:17:41

Input Set : A:\60292668.txt

Output Set : N:\CRF3\03222001\I474980A.raw

```

E--> 327 taccacacgc tgcaagagct gtcggcgagg gagtgcgcggt gcggtgtga      588
4310 <210> SEQ ID NO: 177
4311 <211> LENGTH: 723
4312 <212> TYPE: DNA
4313 <213> ORGANISM: Mus musculus
E--> 4315 <400> SEQUENCE: 153 177<
4316 atggctgcag gaagacattcg gatcctgtgt ctgctgctcc tgtccttgca cccgagcctc      60
4318 ggctgggtcc ttgatcttca agaggcttct gtggcagata agctctcatt tgggaagatg      120
4320 gcagagactc gagggacctg gacgccccat cagggtaaga attcctgggg gcctcccagc      180
4322 tcccacattc cttctctcaa agccctcatc ttgccttaca atcctactct accttgcaact      240
4324 aggtaaccaac catgtccgtc ttccaagacg cttggctgggt tcatgccgac tgtggagcct      300
4326 gaccttacca gtggctgagc tgggcctggg ctatgcctcg gaggagaagg tcatcttccg      360
4328 atactgtgct ggcagctgtc cccaagaggg ccgtaccag cacagtctgg tactggcccg      420
4330 gcttcgaggg cggggtcgag cccatggcgg accctgtgct cagcccacca gctatgctga      480
4332 tgtgaccttc cttgatgacg agcaccattg gcagcagctg cctcagctct cagctgcagc      540
4334 ttgtggctgt ggtggctgaa ggaggccagt ctggtgtctc agaatacaca gcatgagaca      600
4336 ggctgggctt tgaaaggctc aggtgacatt actagaaatt tgcataagta aagataagaa      660
4338 gggaaaggac caggggtttt ttgtttcttt ctttgccttg ttgttagttt tttttttttt      720
4340 ttt
4396 <210> SEQ ID NO: 180
4397 <211> LENGTH: 106 471
4398 <212> TYPE: DNA
4399 <213> ORGANISM: Mus musculus
4401 <400> SEQUENCE: 180
4402 tcagccacca cagccacaag ctgcagctga gagctgaggg agctgctgcc aatgggtgctg      60
4404 atcatcaagg aaggtcacat cagcatagct ggtgggctgg cagcagggtc ggccatgggc      120
4406 tcgaccccg cctcgaagcc gggccagtac cagactgtgc tgggtacggg cctcttgggg      180
4408 acagctgcca gcacagtatc ggaagatgac cttctcctcc gaggcatagc ccaggcccag      240
4410 ctcagccact ggtagggtca ggctccacag tcggcatgaa ccagccaagg ctcttggaag      300
4412 acggacatgg ttgttaccct gatggggcgt ccaggtcctt ctagtctctg ccattctccc      360
4414 aatgagagc ttatctgcca cagaagcctc ttgaagatca aggaccagc cgaggctcgg      420
E--> 4416 gtgcaaggac aggagcagca gacacaggat ccgaagtctt cctgcagcca t      471
5114 <210> SEQ ID NO: 219
5115 <211> LENGTH: 180 23
5116 <212> TYPE: PRT
5117 <213> ORGANISM: Homo sapiens
5119 <400> SEQUENCE: 219
5120 Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
5121 1 5 10 15
5123 Gln Leu Gly Gln Gly Trp Gly
E--> 5124 20
5576 <210> SEQ ID NO: 242
5577 <211> LENGTH: 93
5578 <212> TYPE: PRT
5579 <213> ORGANISM: Mus musculus
5581 <400> SEQUENCE: 242
5582 Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
5583 5 10 15
5585 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/474,980A

DATE: 03/22/2001  
TIME: 16:17:42

Input Set : A:\60292668.txt  
Output Set: N:\CRF3\03222001\I474980A.raw

5586                   20                   25                   30  
5588 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg  
5589                   35                   40                   45  
5591 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro  
5592                   50                   55                   60  
5594 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr  
5595 65                   70                   75                   80  
5597 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys  
5598                   85                   90  
E--> 5601 151  
E--> 5602 24699.doc

*delete*

*see next page for more errors*

09/4/98 4980A 4

<210> 45  
<211> 29  
<212> DNA  
<213> Homo sapiens

*see item 10 on Error Summary Sheet*

<400> 45  
tctctctcrw angcnryngg nckrcarca

29

FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 03/22/2001

PATENT APPLICATION: US/09/474,980A

TIME: 16:17:43

Input Set : A:\60292668.txt

Output Set: N:\CRF3\03222001\I474980A.raw

L:86 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:101 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:106 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:126 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:300 M:252 E: No. of Seq. differs, <211>LENGTH:Input:591 Found:594 SEQ:11  
L:327 M:252 E: No. of Seq. differs, <211>LENGTH:Input:585 Found:588 SEQ:12  
L:688 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33  
L:693 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33  
L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:708 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:713 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:718 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36  
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36  
L:798 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36  
L:803 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36  
L:808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:818 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37  
L:823 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37  
L:828 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37  
L:833 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37  
L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:853 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:858 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:863 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:878 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39  
L:883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39  
L:888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39  
L:893 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39  
L:898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39

## VERIFICATION SUMMARY

DATE: 03/22/2001

PATENT APPLICATION: US/09/474,980A

TIME: 16:17:43

Input Set : A:\60292668.txt

Output Set: N:\CRF3\03222001\I474980A.raw

L:908 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:913 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:918 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:933 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:938 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:943 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:948 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:953 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:958 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:1117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:1215 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:45  
L:1215 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45  
L:1215 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45  
L:1215 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45  
L:1215 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:45  
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L:1472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:1531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:1537 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (51) SEQUENCE:  
L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52  
L:2356 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (104) SEQUENCE:  
L:2442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108  
L:2462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109  
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110  
L:2571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113  
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114  
L:2671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115  
L:2724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116  
L:2782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117  
L:2850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118  
L:2898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119  
L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120  
L:3004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121  
L:3062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122  
L:3130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123  
L:3203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124  
L:3221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125  
L:3256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:126  
L:3276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127  
L:3296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128  
L:3316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129  
L:3341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130  
L:3408 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (133) SEQUENCE:  
L:3525 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:142



VERIFICATION SUMMARY

DATE: 03/22/2001

PATENT APPLICATION: US/09/474,980A

TIME: 16:17:43

Input Set : A:\60292668.txt

Output Set: N:\CRF3\03222001\I474980A.raw

L:3554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:145  
L:4315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:177 differs:153  
L:4416 M:252 E: No. of Seq. differs, <211>LENGTH:Input:106 Found:471 SEQ:180  
L:4922 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5124 M:252 E: No. of Seq. differs, <211>LENGTH:Input:180 Found:23 SEQ:219  
L:5601 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:242  
L:5602 M:333 E: Wrong sequence grouping, Amino acids not in groups!